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RAW SEQUENCE LISTING DATE: 09/17/2004
PATENT APPLICATION: US/10/766,363 **TIME:** 10:37:11

Input Set : N:\CrF3\RULE60\10766363.raw
Output Set: N:\CRF4\09172004\J766363.raw

SEQUENCE LISTING

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45      (D) TOPOLOGY: linear
W--> 46  (ii) MOLECULE TYPE: DNA
47  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
48    CGCCACCGAG GGACCTGAGC GAGTC
50 (2) INFORMATION FOR SEQ ID NO: 2:          25
51  (i) SEQUENCE CHARACTERISTICS:
52    (A) LENGTH: 20 base pairs
53    (B) TYPE: nucleic acid
54    (C) STRANDEDNESS: single
55    (D) TOPOLOGY: linear
W--> 56  (ii) MOLECULE TYPE: DNA
57  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
58    TTCTGGGAAG GGACAGAAGA
60 (2) INFORMATION FOR SEQ ID NO: 3:          20
61  (i) SEQUENCE CHARACTERISTICS:
62    (A) LENGTH: 25 base pairs
63    (B) TYPE: nucleic acid
64    (C) STRANDEDNESS: single
65    (D) TOPOLOGY: linear
W--> 66  (ii) MOLECULE TYPE: DNA
67  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
68    CGCGCTAGCT CTGCCCAAA GAGCT
70 (2) INFORMATION FOR SEQ ID NO: 4:          25
71  (i) SEQUENCE CHARACTERISTICS:
72    (A) LENGTH: 39 base pairs
73    (B) TYPE: nucleic acid
74    (C) STRANDEDNESS: single
75    (D) TOPOLOGY: linear
W--> 76  (ii) MOLECULE TYPE: DNA
77  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
78    CGCGGTACCC TCGAGTCTAG ATATTGCCAG TGGTGGAAAG
80 (2) INFORMATION FOR SEQ ID NO: 5:          39
81  (i) SEQUENCE CHARACTERISTICS:
82    (A) LENGTH: 35 base pairs
83    (B) TYPE: nucleic acid
84    (C) STRANDEDNESS: single
85    (D) TOPOLOGY: linear
W--> 86  (ii) MOLECULE TYPE: DNA
87  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
88    CGTGCAGCCG CTGGAGGACT TTGAGGATGT CTGTC
90 (2) INFORMATION FOR SEQ ID NO: 6:          35
91  (i) SEQUENCE CHARACTERISTICS:
92    (A) LENGTH: 33 base pairs
93    (B) TYPE: nucleic acid
94    (C) STRANDEDNESS: single
95    (D) TOPOLOGY: linear
W--> 96  (ii) MOLECULE TYPE: DNA
97  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
98    CGCTCTAGAG AGACCAGTTA GGAAGTTTC GCA

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100 (2) INFORMATION FOR SEQ ID NO: 7:

101 (i) SEQUENCE CHARACTERISTICS:
102 (A) LENGTH: 2995 base pa
103 (B) TYPE: nucleic acid
104 (C) STRANDEDNESS: single
105 (D) TOPOLOGY: linear

106 (ii) MOLECULE TYPE: cDNA

107 (ix) FEATURE:

108 (A) NAME/KEY: CDS

109 (B) LOCATION: 139..2925

110 (D) OTHER INFORMATION: /product= "RB"

111 /note= "retinoblastoma tumor suppressor"

112 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 113 TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTGTA CGGGAGTCGG GAGAGGACGG
 114 GGC GTGCCCG CCGTGC CGC GC GCG CCTCCACAGC TCGCTGGCTC
 115 CCGCCGCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC
 116 Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
 117 1 5 10
 118 ACC GCC GCC GCT GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC
 119 Thr Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro
 120 15 20 25
 121 CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT
 122 Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro
 123 30 35 40
 124 CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA
 125 Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala
 126 45 50 55
 127 TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG
 128 Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
 129 60 65 70 75
 130 TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT
 131 Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
 132 80 85 90
 133 ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA
 134 Ile Gln Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
 135 95 100 105
 136 GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC
 137 Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
 138 110 115 120
 139 ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT
 140 Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
 141 125 130 135
 142 ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT
 143 Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
 144 140 145 150 155
 145 GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT
 146 Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
 147 160 165 170
 148 ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT
 149 699

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149	Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser		
150	175	180	185
151	GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG		747
152	Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly		
153	190	195	200
154	GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG		795
155	Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met		
156	205	210	215
157	CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC		843
158	Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu		
159	220	225	230
160	235		
161	AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA		891
162	Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg		
163	240	245	250
164	ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA		939
165	Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu		
166	255	260	265
167	GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT		987
168	Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys		
169	270	275	280
170	AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT		1035
171	Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe		
172	285	290	295
173	ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA		1083
174	Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu		
175	300	305	310
176	315		
177	AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA		1131
178	Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu		
179	320	325	330
180	GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT		1179
181	Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser		
182	335	340	345
183	ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT		1227
184	Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp		
185	350	355	360
186	360		
187	GAA GAG GTG AAT GTA ATT CTT CCA CAC ACT CCA GTT AGG ACT GTT ATG		1275
188	Glu Glu Val Asn Val Ile Leu Pro His Thr Pro Val Arg Thr Val Met		
189	365	370	375
190	AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA		1323
191	Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln		
192	380	385	390
193	395		
194	CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA		1371
195	Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro		
196	400	405	410
197	AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA		1419
198	Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys		
199	415	420	425
200	GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA		1467
201	Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser		

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198	430	435	440	
199	CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC			1515
200	Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser			
201	445	450	455	
202	ATG CTT AAA TCA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA			1563
203	Met Leu Lys Ser Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys			
204	460	465	470	475
205	CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT			1611
206	Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu			
207	480	485	490	
208	GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT			1659
209	Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp			
210	495	500	505	
211	TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA			1707
212	Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu			
213	510	515	520	
214	AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA			1755
215	Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu			
216	525	530	535	
217	GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT			1803
218	Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His			
219	540	545	550	555
220	CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT			1851
221	Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp			
222	560	565	570	
223	CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA			1899
224	Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu			
225	575	580	585	
226	TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA			1947
227	Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala			
228	590	595	600	
229	GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT			1995
230	Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr			
231	605	610	615	
232	ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC			2043
233	Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala			
234	620	625	630	635
235	TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT			2091
236	Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr			
237	640	645	650	
238	AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA			2139
239	Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu			
240	655	660	665	
241	CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT			2187
242	Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu			
243	670	675	680	
244	TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT			2235
245	Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His			
246	685	690	695	

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10766363.raw

Output Set: N:\CRF4\09172004\J766363.raw

L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:27 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1) (vi)
L:28 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:31 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)
L:33 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:37 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]
L:46 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:56 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=2
L:66 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:76 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4
L:86 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:96 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6